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Figure 13 is a schematic representation of a method of complexity management comprising hybridizing a probe sequence bound to a magnetic bead to a pool of fractionated DNA, ligating an adaptor sequence containing a class IIs restriction enzyme site to the DNA/probe duplex, digesting the duplex, ligating a second adaptor sequence to the duplex and amplifying.

Figure 14 depicts a chimeric probe array.

Figure 15 is a schematic representation of a method of complexity management comprising hybridizing a probe sequence attached to a magnetic bead to a pool of fractionated DNA, ligating an adaptor sequence containing a class IIs restriction enzyme site to the DNA/probe duplex, digesting the duplex, ligating a second adaptor sequence to the duplex, amplifying and hybridizing the amplicons to a chimeric probe array.

Figure 16 is a schematic representation of a method of complexity management comprising hybridizing a mismatch binding protein to DNA containing a polymorphism and isolating the region containing the polymorphism.

Figure 17 is a schematic representation of a method of complexity management comprising attaching a magnetic bead to the mismatch binding protein of Figure 16.

Exhibit A
~~Exhibit 1~~ is an example of one type of computer program which can be written to model restriction enzyme digestions.

Exhibit B
~~Exhibit 2~~ is an example of one type of computer program which can be written to model ligation reactions.

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DETAILED DESCRIPTION OF THE PRESENT INVENTION

This application relies on the disclosure of other patent applications and literature references. These documents are hereby incorporated by reference in their entireties for all purposes.

Definitions

A "genome" is all the genetic material in the chromosomes of an organism. DNA derived from the genetic material in the chromosomes of a particular organism is genomic